Inventor: Matsui et al.
Title: "ANTIBODIES FOR THE ALPHA PLATELET-DERIVED ..."
Application No.: 10/700,249
Docket No.: 14014.0266u3
REPLACEMENT SHEET

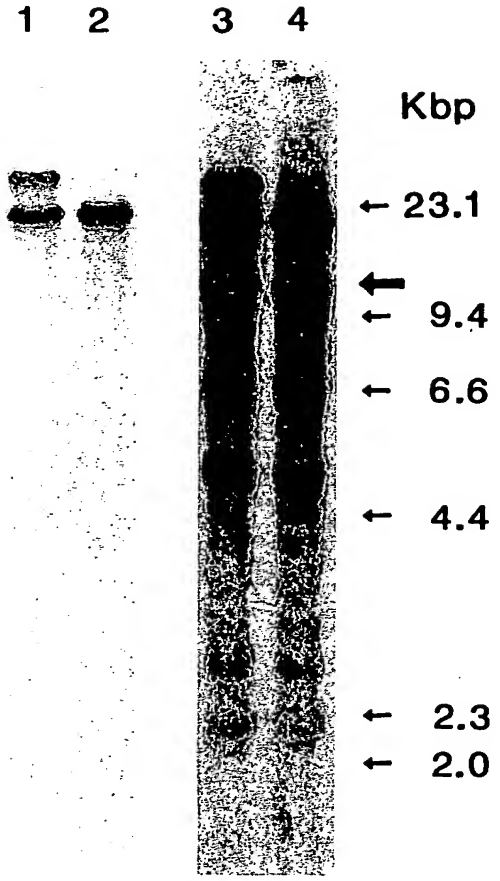


FIG.1A

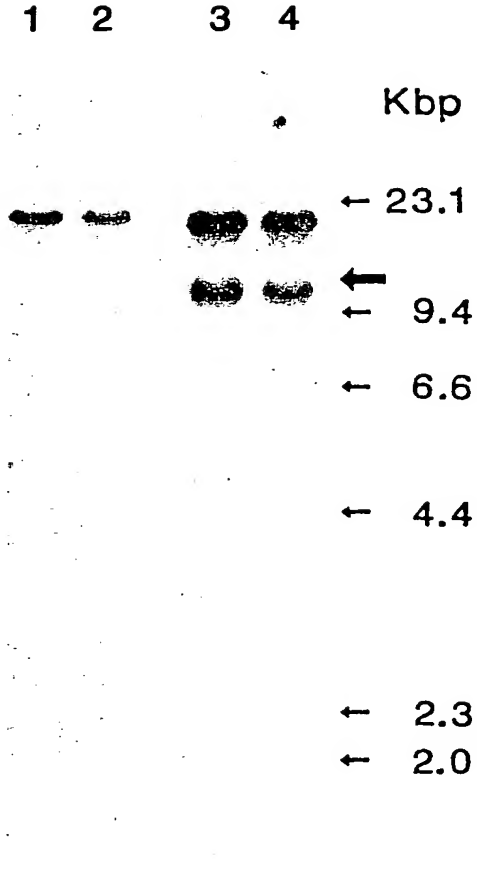
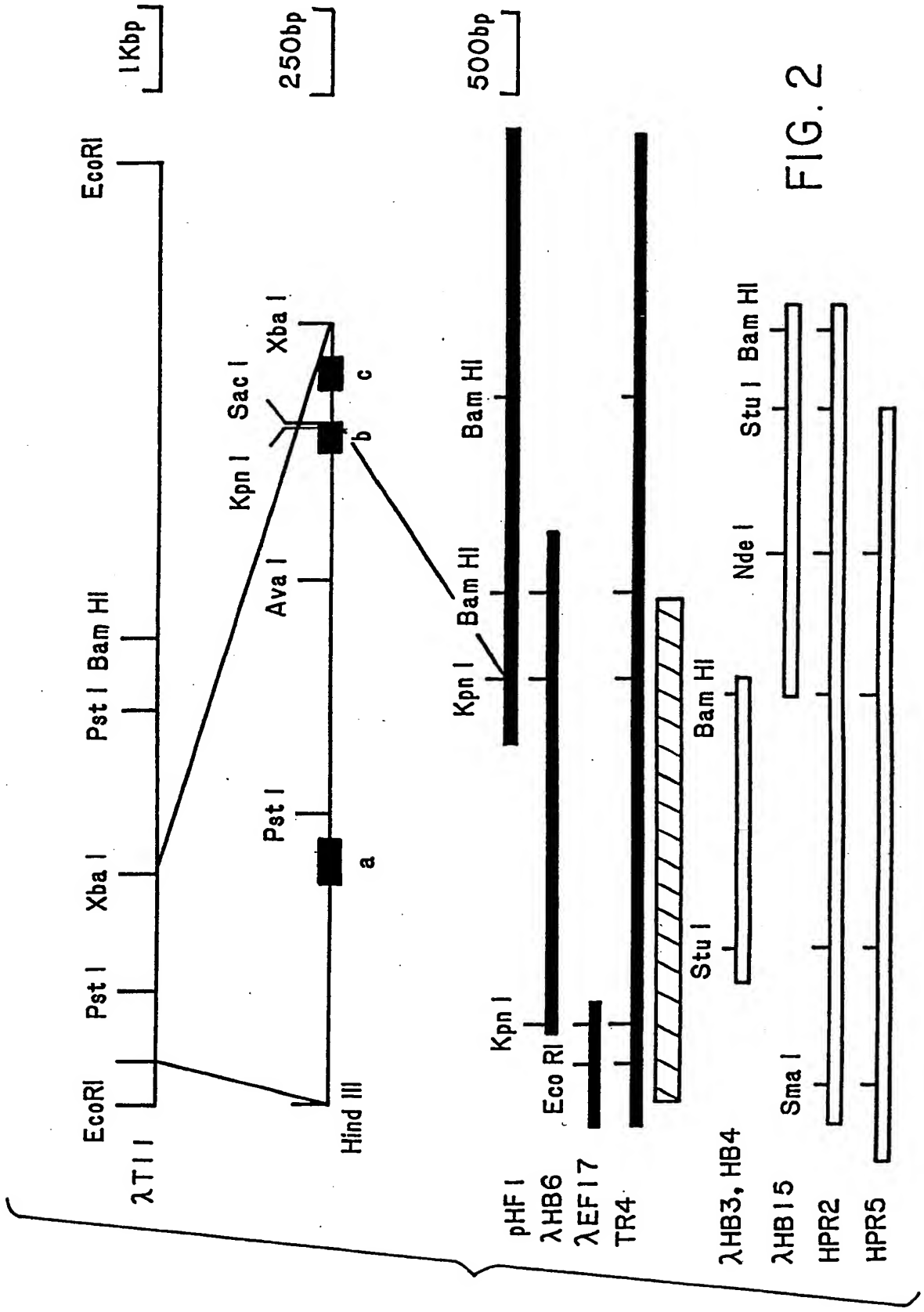


FIG.1B


1Kbp
250bp
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EcoRI
Pst I
Bam HI
Xba I
Pst I
EcoRI
λT11
Kpn I
Sac I
Xba I
Ava I
Pst I
Hind III
a
b
c
Bam HI
Bam HI
Kpn I
Kpn I
Eco RI
Stu I
Bam HI
Nde I
Stu I
Bam HI
Sma I
pHF1
λHB6
λEF17
TR4
λHB3, HB4
λHB15
HPR2
HPR5

FIG. 2

FIG. 3-1

```
   1 CCATTACTGTTGGAGCTACAGGGAGAGAAACAGGAGGAGACTGCAAGAGA

  49 TCATTTGGGAAGGCCGTGGGCACGCTCTTTACTCCATGTGTGGGACATT

                                                      MetGly
 100 CATTGCGGAATAACATCGGAGGAGAAGTTTCCCAGAGCTATGGGG

           5                  10                  15
     ThrSerHisProAlaPheLeuValLeuGlyCysLeuLeuThrGly
 145 ACTTCCCATCCGGCGTTCCTGGTCTTAGGCTGTCTTCTCACAGGG

          20                  25                  30
     LeuSerLeuIleLeuCysGlnLeuSerLeuProSerIleLeuPro
 190 CTGAGCCTAATCCTCTGCCAGCTTTCATTACCCTCTATCCTTCCA

          35                  40                  45
     AsnGluAsnGluLysValValGlnLeuAsnSerSerPheSerLeu
 235 AATGAAAATGAAAAGGTTGTGCAGCTGAATTCATCCTTTTCTCTG

          50                  55                  60
     ArgCysPheGlyGluSerGluValSerTrpGlnTyrProMetSer
 280 AGATGCTTTGGGGAGAGTGAAGTGAGCTGGCAGTACCCCATGTCT

          65                  70                  75
     GluGluGluSerSerAspValGluIleArgAsnGluGluAsnAsn
 325 GAAGAAGAGAGCTCCGATGTGGAAATCAGAAATGAAGAAAACAAC

          80                  85                  90
     SerGlyLeuPheValThrValLeuGluValSerSerAlaSerAla
 370 AGCGGCCTTTTTGTGACGGTCTTGGAAGTGAGCAGTGCCTCGGCG

          95                 100                 105
     AlaHisThrGlyLeuTyrThrCysTyrTyrAsnHisThrGlnThr
 415 GCCCACACAGGGTTGTACACTTGCTATTACAACCACACTCAGACA

         110                 115                 120
     GluGluAsnGluLeuGluGlyArgHisIleTyrIleTyrValPro
 460 GAAGAGAATGAGCTTGAAGGCAGGCACATTTACATCTATGTGCCA

         125                 130                 135
     AspProAspValAlaPheValProLeuGlyMetThrAspTyrLeu
 505 GACCCAGATGTAGCCTTTGTACCTCTAGGAATGACGGATTATTTA
```

FIG. 3-3

```
                320                 325                 330
      LysProThrPheSerGlnLeuGluAlaValAsnLeuHisGluVal
1090  AAACCCACCTTCAGCCAGTTGGAAGCTGTCAACCTGCATGAAGTC

          335                 340                 345
      LysHisPheValValGluValArgAlaTyrProProProArgIle
1135  AAACATTTTGTTGTAGAGGTGCGGGCCTACCCACCTCCCAGGATA

          350                 355                 360
      SerTrpLeuLysAsnAsnLeuThrLeuIleGluAsnLeuThrGlu
1180  TCCTGGCTGAAAAACAATCTGACTCTGATTGAAAATCTCACTGAG

          365                 370                 375
      IleThrThrAspValGluLysIleGlnGluIleArgTyrArgSer
1225  ATCACCACTGATGTGGAAAAGATTCAGGAAATAAGGTATCGAAGC

          380                 385                 390
      LysLeuLysLeuIleArgAlaLysGluGluAspSerGlyHisTyr
1270  AAATTAAAGCTGATCCGTGCTAAGGAAGAAGACAGTGGCCATTAT

          395                 400                 405
      ThrIleValAlaGlnAsnGluAspAlaValLysSerTyrThrPhe
1315  ACTATTGTAGCTCAAAATGAAGATGCTGTGAAGAGCTATACTTTT

          410                 415                 420
      GluLeuLeuThrGlnValProSerSerIleLeuAspLeuValAsp
1360  GAACTGTTAACTCAAGTTCCTTCATCCATTCTGGACTTGGTCGAT

          425                 430                 435
      AspHisHisGlySerThrGlyGlyGlnThrValArgCysThrAla
1405  GATCACCATGGCTCAACTGGGGGACAGACGGTGAGGTGCACAGCT

          440                 445                 450
      GluGlyThrProLeuProAspIleGluTrpMetIleCysLysAsp
1450  GAAGGCACGCCGCTTCCTGATATTGAGTGGATGATATGCAAAGAT

          455                 460                 465
      IleLysLysCysAsnAsnGluThrSerTrpThrIleLeuAlaAsn
1495  ATTAAGAAATGTAATAATGAAACTTCCTGGACTATTTTGGCCAAC

          470                 475                 480
      AsnValSerAsnIleIleThrGluIleHisSerArgAspArgSer
1540  AATGTCTCAAACATCATCACGGAGATCCACTCCCGAGACAGGAGT

          485                 490                 495
      ThrValGluGlyArgValThrPheAlaLysValGluGluThrIle
1585  ACCGTGGAGGGCCGTGTGACTTTCGCCAAAGTGGAGGAGACCATC
```

FIG. 3-4

```
                500                 505                 510
      AlaValArgCysLeuAlaLysAsnLeuLeuGlyAlaGluAsnArg
1630  GCCGTGCGATGCCTGGCTAAGAATCTCCTTGGAGCTGAGAACCGA

                515                 520                 525
      GluLeuLysLeuValAlaProThrLeuArgSerGluLeuThrVal
1675  GAGCTGAAGCTGGTGGCTCCCACCCTGCGTTCTGAACTCACGGTG

                530                 535                 540
      AlaAlaAlaValLeuValLeuLeuValIleValIleIleSerLeu
1720  GCTGCTGCAGTCCTGGTGCTGTTGGTGATTGTGATCATCTCACTT

                545                 550                 555
      IleValLeuValValIleTrpLysGlnLysProArgTyrGluIle
1765  ATTGTCCTGGTTGTCATTTGGAAACAGAAACCGAGGTATGAAATT

                560                 565                 570
      ArgTrpArgValIleGluSerIleSerProAspGlyHisGluTyr
1810  CGCTGGAGGGTCATTGAATCAATCAGCCCGGATGGACATGAATAT

                575                 580                 585
      IleTyrValAspProMetGlnLeuProTyrAspSerArgTrpGlu
1855  ATTTATGTGGACCCGATGCAGCTGCCTTATGACTCAAGATGGGAG

                590                 595                 600
      PheProArgAspGlyLeuValLeuGlyArgValLeuGlySerGly
1900  TTTCCAAGAGATGGACTAGTGCTTGGTCGGGTCTTGGGGTCTGGA

                605                 610                 615
      AlaPheGlyLysValValGluGlyThrAlaTyrGlyLeuSerArg
1945  GCGTTTGGGAAGGTGGTTGAAGGAACAGCCTATGGATTAAGCCGG

                620                 625                 630
      SerGlnProValMetLysValAlaValLysMetLeuLysProThr
1990  TCCCAACCTGTCATGAAAGTTGCAGTGAAGATGCTAAAACCCACG

                635                 640                 645
      AlaArgSerSerGluLysGlnAlaLeuMetSerGluLeuLysIle
2035  GCCAGATCCAGTGAAAAACAAGCTCTCATGTCTGAACTGAAGATA

                650                 655                 660
      MetThrHisLeuGlyProHisLeuAsnIleValAsnLeuLeuGly
2080  ATGACTCACCTGGGGCCACATTTGAACATTGTAAACTTGCTGGGA

                665                 670                 675
      AlaCysThrLysSerGlyProIleTyrIleIleThrGluTyrCys
2125  GCCTGCACCAAGTCAGGCCCCATTTACATCATCACAGAGTATTGC
```

FIG. 3-5

```
                680                 685                 690
          PheTyrGlyAspLeuValAsnTyrLeuHisLysAsnArgAspSer
2170      TTCTATGGAGATTTGGTCAACTATTTGCATAAGAATAGGGATAGC

                695                 700                 705
          PheLeuSerHisHisProGluLysProLysLysGluLeuAspIle
2215      TTCCTGAGCCACCACCCAGAGAAGCCAAAGAAAGAGCTGGATATC

                710                 715                 720
          PheGlyLeuAsnProAlaAspGluSerThrArgSerTyrValIle
2260      TTTGGATTGAACCCTGCTGATGAAAGCACACGGAGCTATGTTATT

                725                 730                 735
          LeuSerPheGluAsnAsnGlyAspTyrMetAspMetLysGlnAla
2305      TTATCTTTTGAAAACAATGGTGACTACATGGACATGAAGCAGGCT

                740                 745                 750
          AspThrThrGlnTyrValProMetLeuGluArgLysGluValSer
2350      GATACTACACAGTATGTCCCCATGCTAGAAAGGAAAGAGGTTTCT

                755                 760                 765
          LysTyrSerAspIleGlnArgSerLeuTyrAspArgProAlaSer
2395      AAATATTCCGACATCCAGAGATCACTCTATGATCGTCCAGCCTCA

                770                 775                 780
          TyrLysLysLysSerMetLeuAspSerGluValLysAsnLeuLeu
2440      TATAAGAAGAAATCTATGTTAGACTCAGAAGTCAAAAACCTCCTT

                785                 790                 795
          SerAspAspAsnSerGluGlyLeuThrLeuLeuAspLeuLeuSer
2485      TCAGATGATAACTCAGAAGGCCTTACTTTATTGGATTTGTTGAGC

                800                 805                 810
          PheThrTyrGlnValAlaArgGlyMetGluPheLeuAlaSerLys
2530      TTCACCTATCAAGTTGCCCGAGGAATGGAGTTTTTGGCTTCAAAA

                815                 820                 825
          AsnCysValHisArgAspLeuAlaAlaArgAsnValLeuLeuAla
2575      AATTGTGTCCACCGTGATCTGGCTGCTCGCAACGTCCTCCTGGCA

                830                 835                 840
          GlnGlyLysIleValLysIleCysAspPheGlyLeuAlaArgAsp
2620      CAAGGAAAAATTGTGAAGATCTGTGACTTTGGCCTGGCCAGAGAC

                845                 850                 855
          IleMetHisAspSerAsnTyrValSerLysGlySerThrPheLeu
2665      ATCATGCATGATTCGAACTATGTGTCGAAAGGCAGTACCTTTCTG
                                                       \_____
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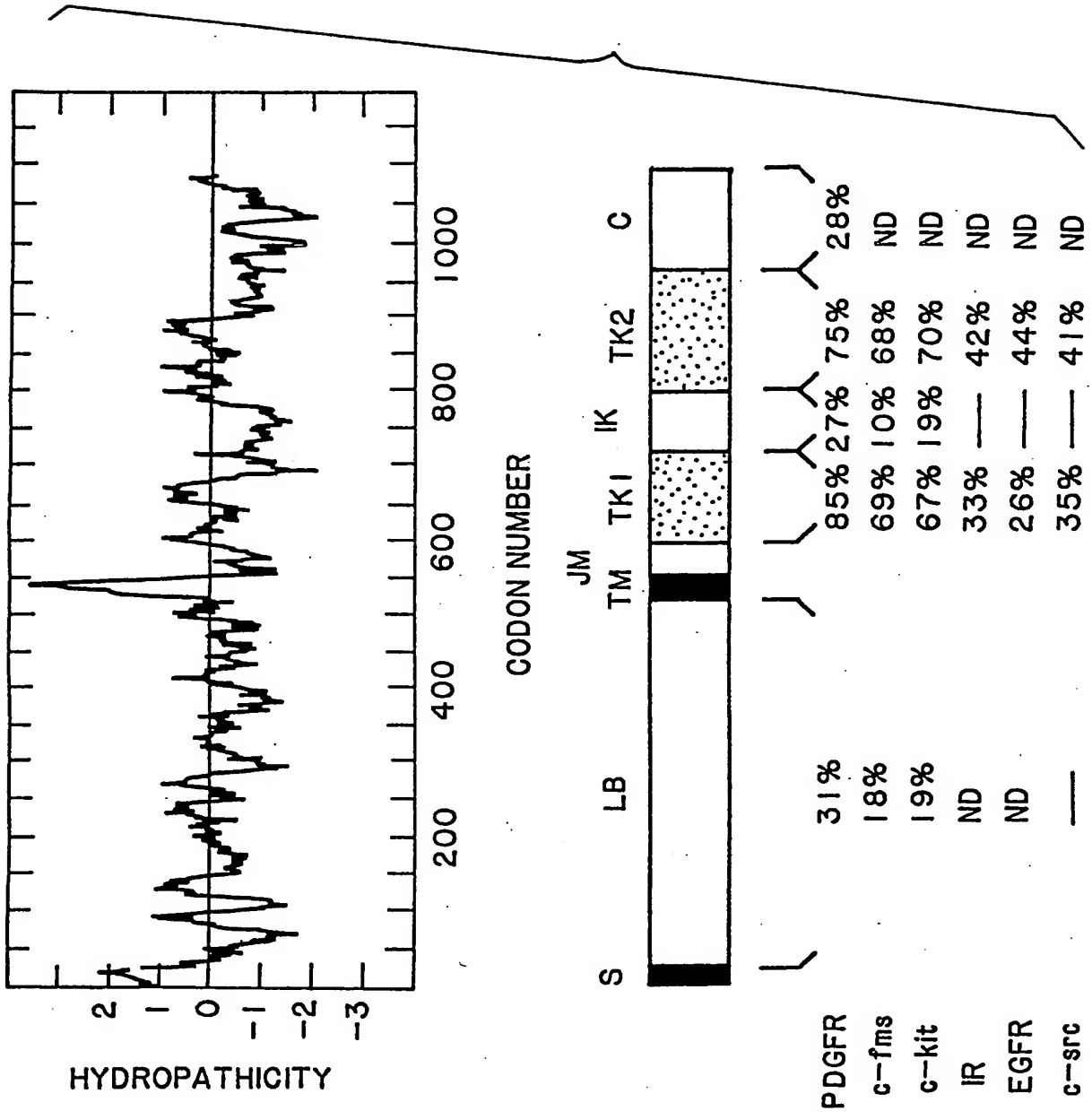
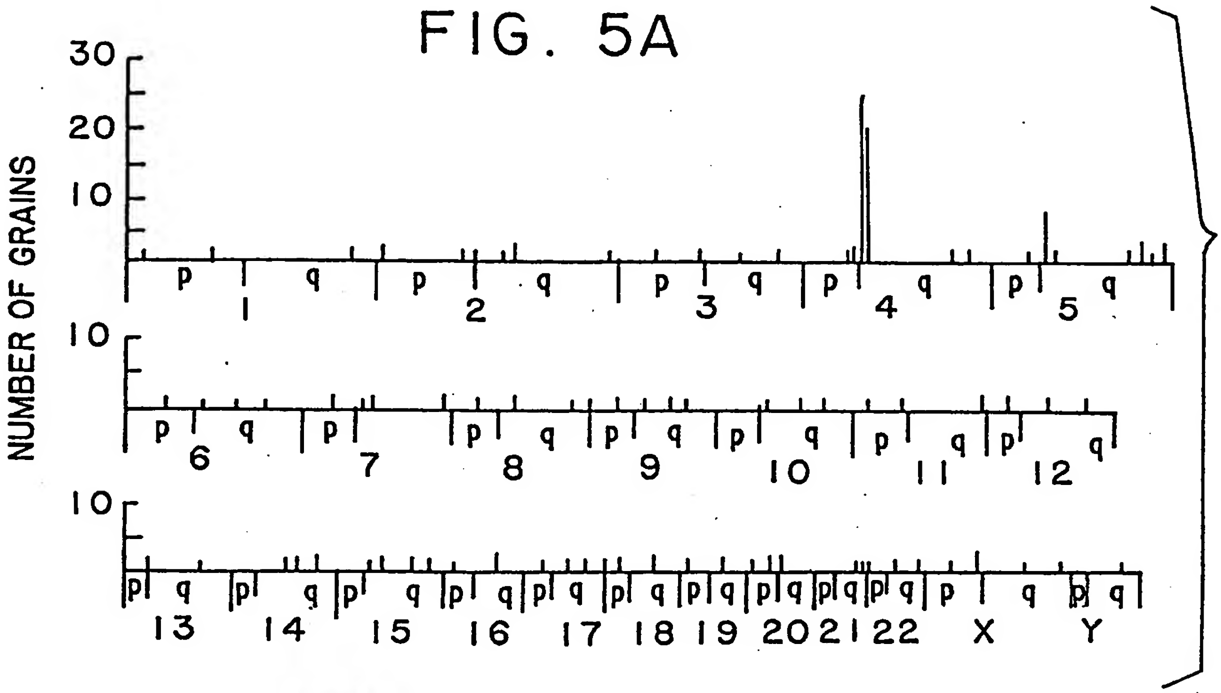

HYDROPATHICITY
2
1
0
-1
-2
-3
200
400
600
800
1000
CODON NUMBER
S
LB
TM
JM
TK1
IK
TK2
C
PDGFR 31% 85% 27% 75% 28%
c-fms 18% 69% 10% 68% ND
c-kit 19% 67% 19% 70% ND
IR ND 33% — 42% ND
EGFR ND 26% — 44% ND
c-src — 35% — 41% ND

FIG. 4

FIG. 5A


NUMBER OF GRAINS
30
20
10
p
1
q
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
X
Y

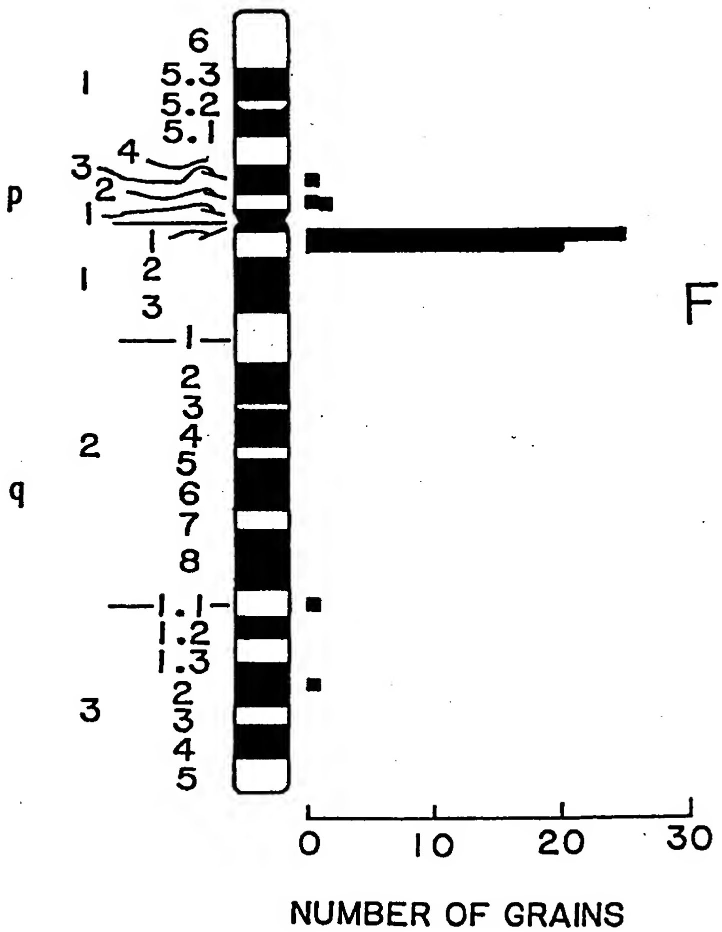

6
5.3
5.2
5.1
p
q
NUMBER OF GRAINS
0
10
20
30

FIG. 5B

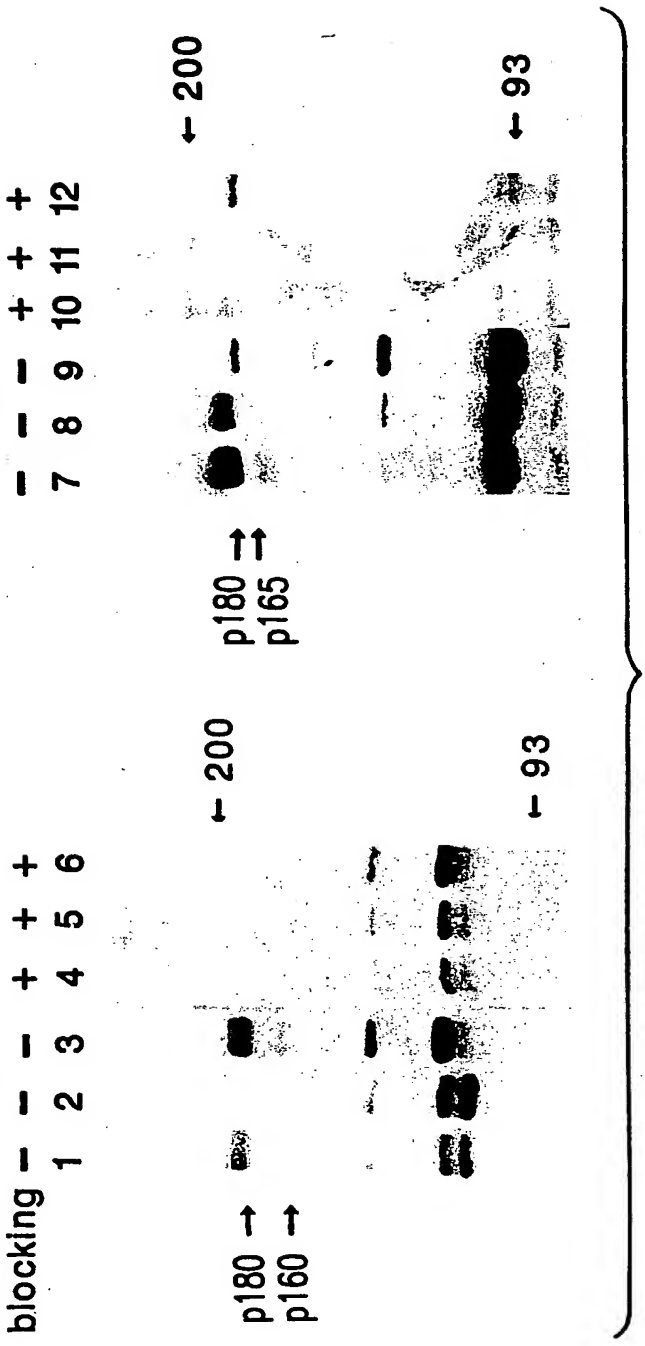

anti-HPR
7 8 9 10 11 12
200
93
p180
p165
anti-T11
blocking - - - + + +
1 2 3 4 5 6
200
93
p180
p160

FIG.7A

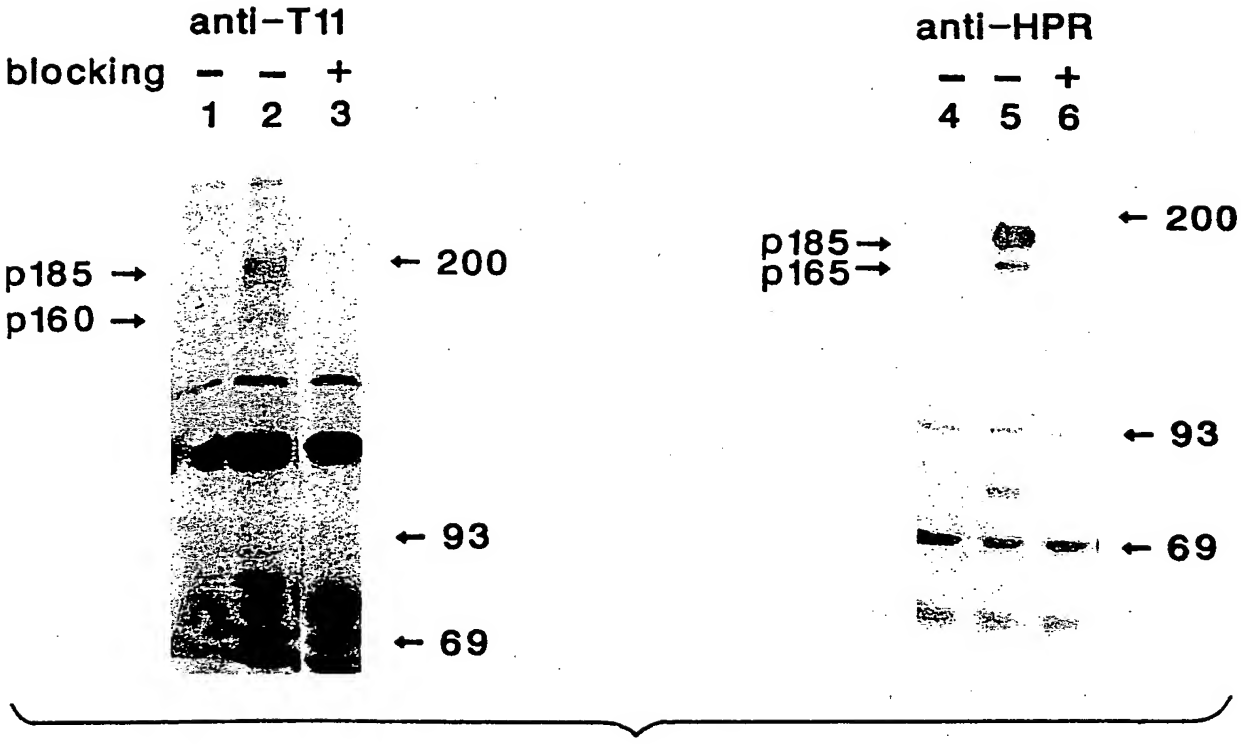

anti-T11
blocking - - +
1 2 3
p185 →
p160 →
← 200
← 93
← 69
anti-HPR
- - +
4 5 6
p185 →
p165 →
← 200
← 93
← 69

FIG.7B

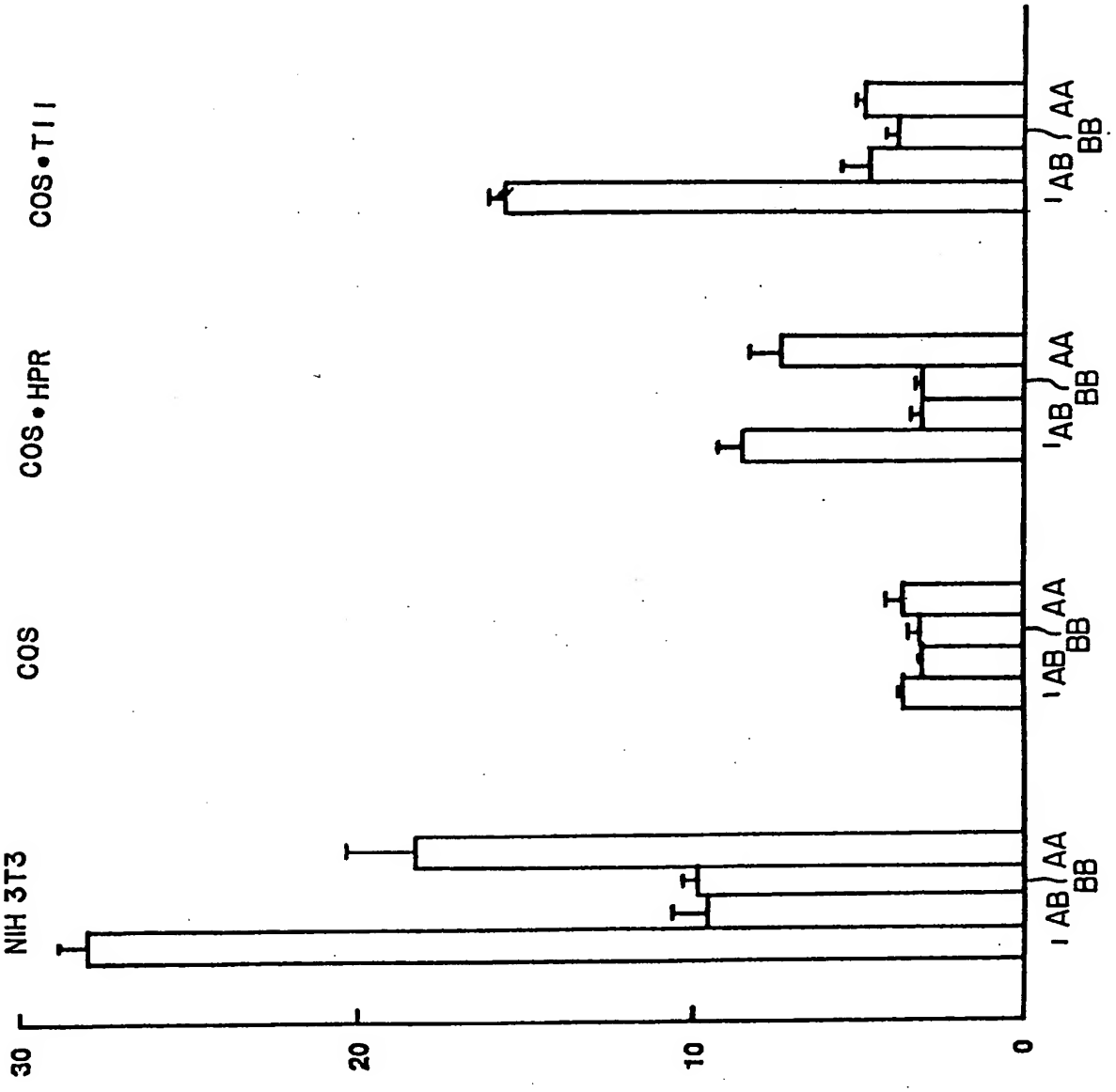

COS • TII
COS • HPR
COS
NIH 3T3
AA
BB
AB
30
20
10
0
^{125}I - Human PDGF binding (cpm x 10^{-2}/well)

FIG. 8

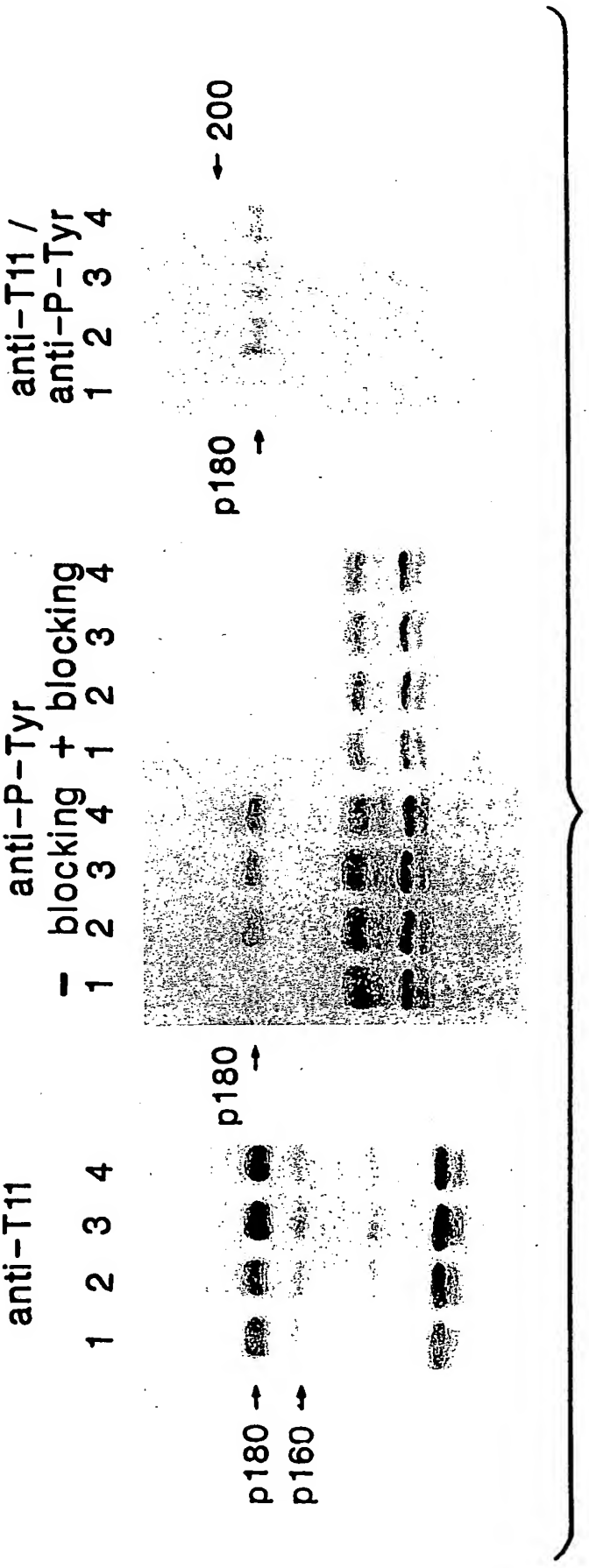

anti-T11
1 2 3 4
p180
p160
anti-P-Tyr
– blocking + blocking
1 2 3 4 1 2 3 4
p180
anti-T11 / anti-P-Tyr
1 2 3 4
200
p180

FIG.9A

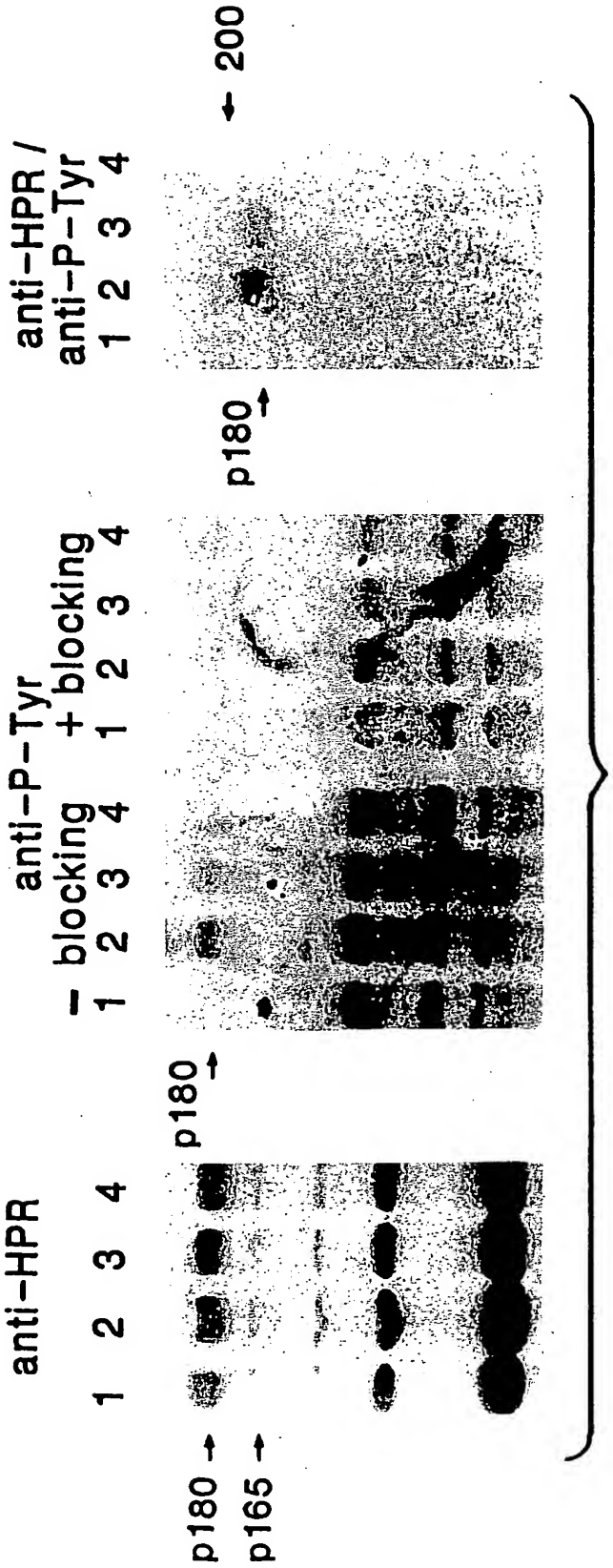

anti-HPR
1 2 3 4
p180
p165
anti-P-Tyr
- blocking + blocking
1 2 3 4 1 2 3 4
p180
anti-HPR / anti-P-Tyr
1 2 3 4
200
p180

FIG.9B

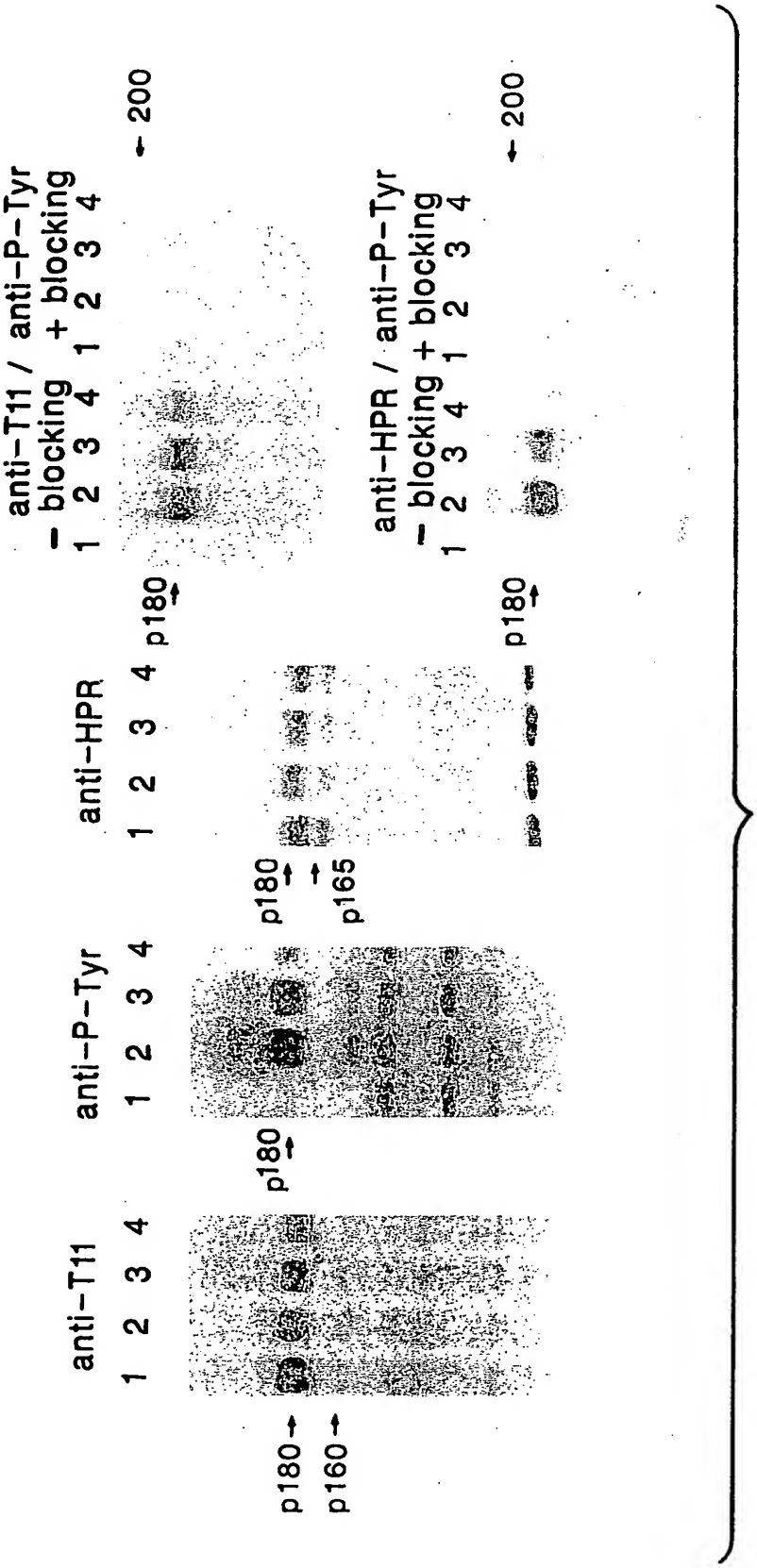

anti-T11
1 2 3 4
p180
p160
anti-P-Tyr
1 2 3 4
p180
anti-HPR
1 2 3 4
p180
p165
anti-T11 / anti-P-Tyr
- blocking + blocking
1 2 3 4 1 2 3 4
200
p180
anti-HPR / anti-P-Tyr
- blocking + blocking
1 2 3 4 1 2 3 4
200
p180

FIG.9C